

WHAT IS CLAIMED IS:

1. Seed of corn inbred line designated D501, representative seed of said line having been deposited under ATCC Accession No. PTA-_____.
2. A corn plant, or a part thereof, produced by growing the seed of claim 1.
3. The corn plant of claim 2, wherein said plant has been detasseled.
4. A tissue culture of regenerable cells produced from the plant of claim 2.
5. Protoplasts produced from the tissue culture of claim 4.
6. The tissue culture of claim 4, wherein cells of the tissue culture are from a tissue selected from the group consisting of leaf, pollen, embryo, root, root tip, anther, silk, flower, kernel, ear, cob, husk and stalk.
7. A corn plant regenerated from the tissue culture of claim 4, said plant having all the morphological and physiological characteristics of inbred line D501, representative seed of said line having been deposited under ATCC Accession No. PTA-_____.
8. A method for producing an F1 hybrid corn seed, comprising crossing the plant of claim 2 with a different corn plant and harvesting the resultant F1 hybrid corn seed.
9. A hybrid corn seed produced by the method of claim 8.
10. A hybrid corn plant, or parts thereof, produced by growing said hybrid seed of claim 9.
11. A method for producing a male sterile corn plant comprising transforming the corn plant of claim 2 with a nucleic acid molecule that confers male sterility.
12. A male sterile corn plant produced by the method of claim 11.
13. A method of producing an herbicide resistant corn plant comprising transforming the corn plant of claim 2 with a transgene that confers herbicide resistance.
14. An herbicide resistant corn plant produced by the method of claim 13.
15. The corn plant of claim 14, wherein the transgene confers resistance to an herbicide selected from the group consisting of: imidazolinone, sulfonylurea, glyphosate, glufosinate, L-phosphinothricin, triazine and benzonitrile.

16. A method of producing an insect resistant corn plant comprising transforming the corn plant of claim 2 with a transgene that confers insect resistance.
17. An insect resistant corn plant produced by the method of claim 16.
18. The corn plant of claim 17, wherein the transgene encodes a *Bacillus thuringiensis* endotoxin.
19. A method of producing a disease resistant corn plant comprising transforming the corn plant of claim 2 with a transgene that confers disease resistance.
20. A disease resistant corn plant produced by the method of claim 19.
21. A method of producing a corn plant with decreased phytate content comprising transforming the corn plant of claim 2 with a transgene encoding phytase.
22. A corn plant with decreased phytate content produced by the method of claim 21.
23. A method of producing a corn plant with modified fatty acid metabolism or modified carbohydrate metabolism comprising transforming the corn plant of claim 2 with a transgene encoding a protein selected from the group consisting of stearyl-ACP desaturase, fructosyltransferase, levansucrase, alpha-amylase, invertase and starch branching enzyme.
24. A corn plant produced by the method of claim 23.
25. The corn plant of claim 24 wherein the transgene confers a trait selected from the group consisting of waxy starch and increased amylose starch.
26. A corn plant, or part thereof, having all the physiological and morphological characteristics of the inbred line D501, representative seed of said line having been deposited under ATCC Accession No. PTA-_____.
27. A method of introducing a desired trait into corn inbred line D501 comprising:
 - (a) crossing D501 plants grown from D501 seed, representative seed of which has been deposited under ATCC Accession No. PTA-_____, with plants of another corn line that comprise a desired trait to produce F1 progeny plants, wherein the desired trait is selected from the group

- consisting of male sterility, herbicide resistance, insect resistance, disease resistance and waxy starch;
- (b) selecting F1 progeny plants that have the desired trait to produce selected F1 progeny plants;
 - (c) crossing the selected progeny plants with the D501 plants to produce backcross progeny plants;
 - (d) selecting for backcross progeny plants that have the desired trait and physiological and morphological characteristics of corn inbred line D501 listed in Table 1 to produce selected backcross progeny plants; and
 - (e) repeating steps (c) and (d) three or more times in succession to produce selected fourth or higher backcross progeny plants that comprise the desired trait and all of the physiological and morphological characteristics of corn inbred line D501 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.

28. A plant produced by the method of claim 27, wherein the plant has the desired trait and all of the physiological and morphological characteristics of corn inbred line D501 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.

29. The plant of claim 28 wherein the desired trait is herbicide resistance and the resistance is conferred to an herbicide selected from the group consisting of: imidazolinone, sulfonylurea, glyphosate, glufosinate, L-phosphinothricin, triazine and benzonitrile.

30. The plant of claim 28 wherein the desired trait is insect resistance and the insect resistance is conferred by a transgene encoding a *Bacillus thuringiensis* endotoxin.

31. The plant of claim 28 wherein the desired trait is male sterility and the trait is conferred by a cytoplasmic nucleic acid molecule that confers male sterility.

32. A method of modifying fatty acid metabolism, modified phytic acid metabolism or modified carbohydrate metabolism into corn inbred line D501 comprising:

- (a) crossing D501 plants grown from D501 seed, representative seed of which has been deposited under ATCC Accession No. PTA-_____, with plants of another corn line that comprise a nucleic acid molecule encoding an enzyme selected from the group consisting of phytase, stearyl-ACP desaturase, fructosyltransferase, levansucrase, alpha-amylase, invertase and starch branching enzyme;
- (b) selecting F1 progeny plants that have said nucleic acid molecule to produce selected F1 progeny plants;
- (c) crossing the selected progeny plants with the D501 plants to produce backcross progeny plants;
- (d) selecting for backcross progeny plants that have said nucleic acid molecule and physiological and morphological characteristics of corn inbred line D501 listed in Table 1 to produce selected backcross progeny plants; and
- (e) repeating steps (c) and (d) three or more times in succession to produce selected fourth or higher backcross progeny plants that comprise said nucleic acid molecule and have all of the physiological and morphological characteristics of corn inbred line D501 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.

33. A plant produced by the method of claim 32, wherein the plant comprises the nucleic acid molecule and has all of the physiological and morphological characteristics of corn inbred line D501 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions.